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RAW SEQUENCE LISTING DATE: 11/13/2001  
PATENT APPLICATION: US/09/919,891 TIME: 15:27:19

Input Set : A:\211714US0X.txt  
Output Set: N:\CRF3\11132001\I919891.raw

3 <110> APPLICANT: BATHE, BRIGITTE  
4 MOCKEL, BETTINA  
5 PFEFFERLE, WALTER  
6 HUTHMACHER, KLAUS  
7 RUCKERT, CHRISTIAN  
8 KALINOWSKI, JORN  
9 PUHLER, ALFRED  
10 BINDER, MICHAEL  
11 GREISSINGER, DIETER  
12 THIERBACH, GEORG  
14 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METH GENE  
16 <130> FILE REFERENCE: 211714US0X  
18 <140> CURRENT APPLICATION NUMBER: 09/919,891  
19 <141> CURRENT FILING DATE: 2001-08-02  
21 <150> PRIOR APPLICATION NUMBER: DE 10038050.6  
22 <151> PRIOR FILING DATE: 2000-08-02  
24 <150> PRIOR APPLICATION NUMBER: DE 10109687.9  
25 <151> PRIOR FILING DATE: 2001-02-28  
27 <150> PRIOR APPLICATION NUMBER: US 60/294,251  
28 <151> PRIOR FILING DATE: 2001-05-31  
30 <160> NUMBER OF SEQ ID NOS: 4  
32 <170> SOFTWARE: PatentIn version 3.1  
34 <210> SEQ ID NO: 1  
35 <211> LENGTH: 4301  
36 <212> TYPE: DNA  
37 <213> ORGANISM: Corynebacterium glutamicum  
39 <220> FEATURE:  
40 <221> NAME/KEY: CDS  
41 <222> LOCATION: (385)..(4047)  
42 <223> OTHER INFORMATION:  
45 <400> SEQUENCE: 1

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50	tgtccacat gtgtttcg atgtgggtgt gagtccaaga ggtggcttt acgtcgtaaa	180
52	gcaattttag ccactctcc cacggcttc cggtgccgtt gagatagct tcaggggaca	240
54	tgcctggtgt tgagcctgc ggagtggagt cagtcatgc accgagacta gtggcgcttt	300
56	gcctgtgttg cttagggcgc gttaaaatg aactacgaat gaaaagttcg ggaattgtct	360
58	aatccgtact aagctgtcta caca atg tct act tca gtt act tca cca gcc	411
59	Met Ser Thr Ser Val Thr Ser Pro Ala	
60	1 5	
62	cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg ttg gca aac cat	459
63	His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala Leu Ala Asn His	
64	10 15 20 25	
66	gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc caa ggc ttt gac	507
67	Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu Gln Gly Phe Asp	
68	30 35 40	
70	ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg tgt aat gag att	555

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72			45					50					55						
74	ctc	aac	gac	acc	cgc	cct	gat	gtg	ttg	agg	cag	att	cac	cgc	gcc	tac	603		
75	Leu	Asn	Asp	Thr	Arg	Pro	Asp	Val	Leu	Arg	Gln	Ile	His	Arg	Ala	Tyr			
76			60					65				70							
78	ttt	gag	gcg	gga	gct	gac	ttg	gtt	gag	acc	aat	act	ttt	ggt	tgc	aac	651		
79	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr	Phe	Gly	Cys	Asn			
80		75				80					85								
82	ctg	ccg	aac	ttg	gcg	gat	tat	gac	atc	gct	gat	cgt	tgc	cgt	gag	ctt	699		
83	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu			
84	90				95					100				105					
86	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	gat	gag	atg	ggg	747		
87	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly			
88					110				115				120						
90	ccg	ggc	cga	aac	ggc	atg	cg	cg	ttc	gtg	gtt	gg	tcc	ctg	gga	cct	795		
91	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	Ser	Leu	Gly	Pro			
92					125				130				135						
94	gga	acg	aag	ttt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	gca	gat	ttg	cgt	843		
95	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg			
96					140				145				150						
98	ggg	cac	tac	aag	gaa	gca	g	cg	ttt	ggc	atc	atc	gac	g	gtt	ggc	gat	891	
99	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	Gly	Gly	Gly	Asp			
100					155				160				165						
102	gcc	ttt	ttg	att	gag	act	g	c	tg	atc	g	ac	t	tc	g	tc	939		
103	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala			
104	170					175				180				185					
106	gtt	cac	ggc	gtt	caa	gat	g	cc	atg	g	ctt	gat	aca	t	tc	ttg	987		
107	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro			
108					190				195				200						
110	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	atg	ctc	atg	ggt	1035		
111	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly			
112					205				210				215						
114	tct	gag	atc	ggt	gcc	g	cg	ttt	aca	g	cg	ctg	c	tg	gg	atc	gac	1083	
115	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp			
116					220				225				230						
118	atg	att	ggt	ctg	aac	tgc	g	cc	acc	ggc	cca	gat	g	ag	atg	agc	gag	1131	
119	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His			
120					235				240				245						
122	ctg	cgt	tac	ctg	tcc	aag	cac	g	cc	gat	att	c	ct	gt	tc	tg	1179		
123	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro			
124	250					255				260				265					
126	aac	gca	ggt	ctt	cct	gtc	ctg	gg	aaa	aac	gg	gca	gaa	tac	cc	tt	1227		
127	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu			
128					270				275				280						
130	gag	g	c	t	g	at	tt	g	cg	c	g	ct	g	t	cc	g	aa	tat	1275
131	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr			
132					285				290				295						
134	ggc	ctg	tcc	atg	gt	gg	gt	gt	tgt	gg	gc	acc	ac	c	tc	g	ac	atc	1323
135	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile			

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138	cgt	gcf	gtc	cgf	gat	gcf	gtg	gtt	ggt	gtt	cca	gag	cag	gaa	acc	tcc	1371
139	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	
140	315		320								325						
142	aca	ctg	acc	aag	atc	cct	gca	ggc	cct	gtt	gag	cag	gcc	tcc	cgc	gag	1419
143	Thr	Leu	Thr	Lys	Ile	Pro	Ala	Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	
144	330		335								340					345	
146	gtg	gag	aaa	gag	gac	tcc	gtc	gcf	tcg	ctg	tac	acc	tcg	gtg	cca	ttg	1467
147	Val	Glu	Lys	Glu	Asp	Ser	Val	Ala	Ser	Leu	Tyr	Thr	Ser	Val	Pro	Leu	
148	350		355								360						
150	tcc	cag	gaa	acc	ggc	att	tcc	atg	atc	ggt	gag	cgc	acc	aac	tcc	aac	1515
151	Ser	Gln	Glu	Thr	Gly	Ile	Ser	Met	Ile	Gly	Glu	Arg	Thr	Asn	Ser	Asn	
152	365		370								375						
154	ggt	tcc	aag	gca	ttc	cgt	gag	gca	atg	ctg	tct	ggc	gat	tgg	gaa	aag	1563
155	Gly	Ser	Lys	Ala	Phe	Arg	Glu	Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	
156	380		385								390						
158	tgt	gtg	gat	att	gcc	aag	cag	caa	acc	cgc	gat	ggt	gca	cac	atg	ctg	1611
159	Cys	Val	Asp	Ile	Ala	Lys	Gln	Gln	Thr	Arg	Asp	Gly	Ala	His	Met	Leu	
160	395		400								405						
162	gat	ctt	tgt	gtg	gat	tac	gtg	gga	cga	gac	ggc	acc	gcc	gat	atg	gcf	1659
163	Asp	Leu	Cys	Val	Asp	Tyr	Val	Gly	Arg	Asp	Gly	Thr	Ala	Asp	Met	Ala	
164	410		415								420					425	
166	acc	ttg	gca	gca	ctt	ctt	gct	acc	agc	tcc	act	ttg	cca	atc	atg	att	1707
167	Thr	Leu	Ala	Ala	Leu	Leu	Ala	Thr	Ser	Ser	Thr	Leu	Pro	Ile	Met	Ile	
168	430		435								440						
170	gac	tcc	acc	gag	cca	gag	gtt	att	cgc	aca	ggc	ctt	gag	cac	ttg	ggt	1755
171	Asp	Ser	Thr	Glu	Pro	Glu	Val	Ile	Arg	Thr	Gly	Leu	Glu	His	Leu	Gly	
172	445		450								455						
174	gga	cga	agc	atc	gtt	aac	tcc	gtc	aat	ttt	gaa	gac	ggc	gat	ggc	cct	1803
175	Gly	Arg	Ser	Ile	Val	Asn	Ser	Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	
176	460		465								470						
178	gag	tcc	cgf	tac	cag	cgf	atc	atg	aaa	ctg	gta	aag	cag	cac	ggt	gcf	1851
179	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	Met	Lys	Leu	Val	Lys	Gln	His	Gly	Ala	
180	475		480								485						
182	gcc	gtg	gtt	gcf	ctg	acc	att	gat	gag	gaa	ggc	cag	gca	cgt	acc	gct	1899
183	Ala	Val	Val	Ala	Leu	Thr	Ile	Asp	Glu	Glu	Gly	Gln	Ala	Arg	Thr	Ala	
184	490		495								500					505	
186	gag	cac	aag	gtg	cgf	att	gct	aaa	cga	ctg	att	gac	gat	atc	acc	ggc	1947
187	Glu	His	Lys	Val	Arg	Ile	Ala	Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	
188	510		515								520						
190	agc	tac	ggc	ctg	gat	atc	aaa	gac	atc	gtt	gtg	gac	tgc	ctg	acc	ttc	1995
191	Ser	Tyr	Gly	Leu	Asp	Ile	Lys	Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	
192	525		530								535						
194	ccg	atc	tct	act	ggc	cag	gaa	gaa	acc	agg	cga	gat	ggc	att	gaa	acc	2043
195	Pro	Ile	Ser	Thr	Gly	Gln	Glu	Glu	Thr	Arg	Arg	Asp	Gly	Ile	Glu	Thr	
196	540		545								550						
198	atc	gaa	gcc	atc	cgf	gag	ctg	aag	aag	ctc	tac	cca	gaa	atc	cac	acc	2091
199	Ile	Glu	Ala	Ile	Arg	Glu	Leu	Lys	Lys	Leu	Tyr	Pro	Glu	Ile	His	Thr	
200	555		560								565						

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203 Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn Pro Ala Ala Arg	
204 570 575 580 585	
206 cag gtt ctt aac tct gtg ttc ctc aat gag tgc att gag gct ggt ctg	2187
207 Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile Glu Ala Gly Leu	
208 590 595 600	
210 gac tct gcg att gcg cac agc tcc aag att ttg ccg atg aac cgc att	2235
211 Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro Met Asn Arg Ile	
212 605 610 615	
214 gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc tat gat cgc cgc	2283
215 Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val Tyr Asp Arg Arg	
216 620 625 630	
218 acc gag gat tac gat ccg ctg cag gaa ttc atg cag ctg ttt gag ggc	2331
219 Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln Leu Phe Glu Gly	
220 635 640 645	
222 gtt tct gct gcc gat gcc aag gat gct cgc gct gaa cag ctg gcc gct	2379
223 Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu Gln Leu Ala Ala	
224 650 655 660 665	
226 atg cct ttg ttt gag cgt ttg gca cag cgc atc atc gac ggc gat aag	2427
227 Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile Asp Gly Asp Lys	
228 670 675 680	
230 aat ggc ctt gag gat gat ctg gaa gca ggc atg aag gag aag tct cct	2475
231 Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys Glu Lys Ser Pro	
232 685 690 695	
234 att gcg atc atc aac gag gac ctt ctc aac ggc atg aag acc gtc ggt	2523
235 Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met Lys Thr Val Gly	
236 700 705 710	
238 gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc gtc ctg caa tcg	2571
239 Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser	
240 715 720 725	
242 gca gaa acc atg aaa act gcg gtc gcc tat ttg gaa ccg ttc atg gaa	2619
243 Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu Pro Phe Met Glu	
244 730 735 740 745	
246 gag gaa gca gaa gct acc gga tct gcg cag gca gag ggc aag ggc aaa	2667
247 Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu Gly Lys Gly Lys	
248 750 755 760	
250 atc gtc gtc gcc acc gtc aag ggt gac gtc cac gat atc ggc aag aac	2715
251 Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn	
252 765 770 775	
254 ttg gtc gac atc att ttg tcc aac aac ggt tac gac gtc gtc aac ttg	2763
255 Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp Val Val Asn Leu	
256 780 785 790	
258 ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca gcg gaa gaa cac	2811
259 Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala Ala Glu Glu His	
260 795 800 805	
262 aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtc aag tcc acc gtc	2859
263 Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val Lys Ser Thr Val	
264 810 815 820 825	
266 gtc atg aag gaa aac ctt gag gag atg aac aac gcc ggc gca tcc aat	2907

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270 tac cca gtc att ttg, ggt ggc gct gcg ctg acg cgt acc tac gtg gaa	2955
271 Tyr Pro Val Ile Leu Gly Gly Ala Ala Leu Thr Arg Thr Tyr Val Glu	
272                       845                       850                       855	
274 aac gat ctc aac gag gtg tac acc ggt gag gtg tac tac gcc cgt gat	3003
275 Asn Asp Leu Asn Glu Val Tyr Thr Gly Glu Val Tyr Tyr Ala Arg Asp	
276                       860                       865                       870	
278 gct ttc gag ggc ctg cgc ctg atg gat gag gtg atg gca gaa aag cgt	3051
279 Ala Phe Glu Gly Leu Arg Leu Met Asp Glu Val Met Ala Glu Lys Arg	
280                       875                       880                       885	
282 ggt gaa gga ctt gat ccc aac tca cca gaa gct att gag cag gcg aag	3099
283 Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu Gln Ala Lys	
284 890                       895                       900                       905	
286 aag aag gcg gaa cgt aag gct cgt aat gag cgt tcc cgc aag att gcc	3147
287 Lys Lys Ala Glu Arg Lys Ala Arg Asn Glu Arg Ser Arg Lys Ile Ala	
288                       910                       915                       920	
290 gcg gag cgt aaa gct aat gcg gct ccc gtg att gtt ccg gag cgt tct	3195
291 Ala Glu Arg Lys Ala Asn Ala Ala Pro Val Ile Val Pro Glu Arg Ser	
292                       925                       930                       935	
294 gat gtc tcc acc gat act cca acc gcg gca cca ccg ttc tgg gga acc	3243
295 Asp Val Ser Thr Asp Thr Pro Thr Ala Ala Pro Pro Phe Trp Gly Thr	
296                       940                       945                       950	
298 cgc att gtc aag ggt ctg ccc ttg gcg gag ttc ttg ggc aac ctt gat	3291
299 Arg Ile Val Lys Gly Leu Pro Leu Ala Glu Phe Leu Gly Asn Leu Asp	
300                       955                       960                       965	
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303 Glu Arg Ala Leu Phe Met Gly Gln Trp Gly Leu Lys Ser Thr Arg Gly	
304 970                       975                       980                       985	
306 aac gag ggt cca agc tat gag gat ttg gtg gaa act gaa ggc cga cca	3387
307 Asn Glu Gly Pro Ser Tyr Glu Asp Leu Val Glu Thr Glu Gly Arg Pro	
308                       990                       995                       1000	
310 cgc ctg cgc tac tgg ctg gat cgc ctg aag tct gag ggc att ttg	3432
311 Arg Leu Arg Tyr Trp Leu Asp Arg Leu Lys Ser Glu Gly Ile Leu	
312                       1005                       1010                       1015	
314 gac cac gtg gcc ttg gtg tat ggc tac ttc cca gcg gtc gcg gaa	3477
315 Asp His Val Ala Leu Val Tyr Gly Tyr Phe Pro Ala Val Ala Glu	
316                       1020                       1025                       1030	
318 ggc gat gac gtg gtg atc ttg gaa tcc ccg gat cca cac gca gcc	3522
319 Gly Asp Asp Val Val Ile Leu Glu Ser Pro Asp Pro His Ala Ala	
320                       1035                       1040                       1045	
322 gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc	3567
323 Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe	
324                       1050                       1055                       1060	
326 ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag	3612
327 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys	
328                       1065                       1070                       1075	
330 gac ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt	3657
331 Asp Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly	

**VERIFICATION SUMMARY**

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